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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/805,805	03/13/2001	Shuqian Jing	MBHB01-006-A1	6328

20306 7590 01/15/2003

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EXAMINER	
ROMEO, DAVID S	
ART UNIT	PAPER NUMBER
1647	8

DATE MAILED: 01/15/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/805,805	JING ET AL.	
	Examiner	Art Unit	
	David S Romeo	1647	

-- The MAILING DATE of this communication appears on th cov r sheet with th corr spondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *25 October 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-54* is/are pending in the application.

4a) Of the above claim(s) *9,12-43 and 45-54* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-8,10,11 and 44* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) *1-54* are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *5* .
4) ☒ Interview Summary (PTO-413) Paper No(s). *5* .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Claims 1-54 are pending.

Applicant's election with traverse of group I, claims 1-8, 10, 11, in Paper No. 7 is acknowledged. The traversal is on the ground(s) that claim 44 is not distinct from group I, and that groups A and B are not distinct. This is found persuasive in part. Claim 44 will be joined with group I and groups A and B will be examined to the extent that they are drawn to or encompass claims 1-8, 10, 11, 44 and an isolated nucleic acid molecule encoding the amino acid sequence of SEQ ID NO: 2.

The requirement is still deemed proper and is therefore made FINAL.

Claims 9, 12-43, 45-54 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in Paper No. 7.

Claims 1-8, 10, 11, 44 are being examined.

Based on an inspection of the 60/188,786 parent provisional application, the examiner has concluded that SEQ ID NO: 1, ATCC deposit no. PTA-1882, and 70 percent identical in the present application are not supported by the disclosure in the 60/188,786 parent provisional application because SEQ ID NO: 1, ATCC deposit no. PTA-1882, and 70 percent identical are not disclosed in the manner provided by 35 U.S.C. 112, first paragraph, in the 60/188,786 parent

provisional application. Accordingly, the subject matter defined in claims 1, 2, 4-8, 10, 11, 44 has an effective filing date of 03/13/2001.

Should the applicant disagree with the examiner's determination above, it is incumbent upon the applicant to provide the specific page number(s) in the parent application filed prior to 03/13/2001 which specifically supports these particular claim limitations, and which applicant considers to have been in possession of and fully enabled for prior to 03/13/2001.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-8, 10, 11, 44 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The specification lacks complete deposit information for the deposit of ATCC deposit no. PTA-1882. While the specification provides enough information for one of skill in the art to produce a polynucleotide comprising a coding sequence with the same or similar properties as, reproduction of an identical polynucleotide is a highly unpredictable event. Because it does not appear that ATCC deposit no. PTA-1882 is known and publicly available or can be reproducibly isolated from nature without undue experimentation and because the claims require the use of ATCC deposit no. PTA-1882, a suitable deposit of the clones is required for patent purposes.

Applicants referral to the deposit of ATCC deposit no. PTA-1882 at page 77 is insufficient to ensure that all of the conditions of 37 CFR § 1.801-1.809 have been met. If the deposit was made under the provision of the Budapest Treaty, filing of an affidavit or declaration by applicants or assignees, or a statement by an attorney of record over his or her signature and registration number, stating that the deposit has been accepted by an International Depository Authority under the provisions of the Budapest Treaty, that all restrictions upon public access to the deposit will be irrevocably removed upon the grant of a patent on this application and that the deposit will be replaced if viable samples cannot be dispensed by the depository, is required. This requirement is necessary when a deposit is made under the provisions of the Budapest Treaty as the treaty leaves these specific matters to the discretion of each State. Amendment of the specification to recite the date of the deposit and the complete name and address of the depository, and amendment of the claims to refer to the accession number, is required. In addition, claims reciting the deposited material must be amended to include the depository accession number of the deposited material. Furthermore, unless the deposit was made at or before the time of filing, a declaration under 37 CFR 1.132 is necessary to construct a chain of custody. The declaration, executed by a person in a position to know, should identify the deposited clones by its depository accession number, establish that the deposited clones are the same as that described in the specification and establish that the deposited clone was in applicants' possession at the time of filing. The new address for the ATCC, effective March 23, 1998, is American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209.

Claims 1-8, 10, 11, 44 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The present specification discloses polynucleotides encoding the amino acid sequence of SEQ ID NO: 2 and exemplifies such a polynucleotide with SEQ ID NO: 1. The claims are directed to or encompass nucleic acid molecules that hybridize to the complement of such polynucleotides, or to polynucleotide variants of such polynucleotides, or to polynucleotides encoding variants of SEQ ID NO: 2; nucleic acid molecules encoding a polypeptide having a percent identity to the amino acid sequence of SEQ ID NO: 2; nucleic acid molecules comprising allelic or splice variants of polynucleotides encoding SEQ ID NO: 2, or other variants of polynucleotides encoding variants of SEQ ID NO: 2; nucleic acid molecules comprising fragments of polynucleotides encoding fragments of SEQ ID NO: 2; nucleic acid molecules encoding conservatively or non-conservatively amino acid substituted, inserted, or deleted variants of SEQ ID NO: 2. This rejection is meant to encompass any and/or all embodiments of the claims other than a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1 or the nucleotide sequence of the insert of the deposited clone, or a nucleic acid molecule encoding the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence encoded by the deposited clone.

In some instances the claims require that the polypeptide encoded by the claimed nucleic acid molecule possess an activity that is possessed by the polypeptide of SEQ ID NO: 2 or possess antigenic properties. However, the claims do not require that the polypeptide possess any particular biological activity, nor any particular conserved structure, or other disclosed

distinguishing feature. Simply describing a large genus of any and/or all potential activities, as in, "an activity that is possessed by the polypeptide of SEQ ID NO: 2", is not sufficient to satisfy the written description requirement as to a particular biological activity. Nor does such a description lead those skilled in the art to a particular activity. The property of being "antigenic" says nothing regarding the particular antigenicity of the polypeptide or fragment. Thus, the claims are drawn to a genus of nucleic acid molecules encoding a genus of variant polypeptides that is specifically defined only by some level of nucleotide or amino acid sequence similarity. The specification and claim do not indicate what distinguishing attributes shared by the members of the genus. In some cases, the specification and claim do not place any limit on the number of amino acid substitutions, deletions, insertions and/or additions that may be made to SEQ ID NO: 2. In some cases, the specification and claim do not place any limit on the number of nucleotide substitutions, deletions, insertions and/or additions that may be made to SEQ ID NO: 1 or to polynucleotides encoding SEQ ID NO: 2. The specification and claim do not provide any guidance as to what changes should be made. Structural features that could distinguish compounds in the genus from others in the protein class are missing from the disclosure. No common structural attributes identify the members of the genus. The general knowledge and level of skill in the art do not supplement the omitted description because specific, not general, guidance is what is needed. Since the disclosure fails to describe the common attributes or characteristics that identify members of the genus and because the genus is highly variant, SEQ ID NO: 1 and polynucleotides encoding SEQ ID NO: 2, alone, are insufficient to describe the genus. One of skill in the art would reasonably conclude that the disclosure fails to provide a

representative number of species to describe the genus. Thus, applicant was not in possession of the claimed genus.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of compete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure in the form of some level of amino acid or nucleotide sequence identity. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus. Applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the written description inquiry, whatever is now claimed. The specification does not clearly allow persons of ordinary skill in the art to recognize that Applicants invented what is claimed. The skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polynucleotides and/or polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of making or isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating or making it. The compound itself is required. One cannot describe what one has not conceived. Therefore, only nucleic acid molecules comprising the nucleotide sequence of SEQ ID NO: 1 or nucleic acid molecules

encoding the amino acid sequence of SEQ ID NO: 2, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that the written description provision of 35 U.S.C. §112 is severable from its enablement provision.

Claims 1-8, 10, 11, 44 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. .

The claims are directed to or encompass nucleic acid molecules that hybridize to the complement of such polynucleotides, or to polynucleotide variants of such polynucleotides, or to polynucleotides encoding variants of SEQ ID NO: 2; nucleic acid molecules encoding a polypeptide having a percent identity to the amino acid sequence of SEQ ID NO: 2; nucleic acid molecules comprising allelic or splice variants of polynucleotides encoding SEQ ID NO: 2, or other variants of polynucleotides encoding variants of SEQ ID NO: 2; nucleic acid molecules comprising fragments of polynucleotides encoding fragments of SEQ ID NO: 2; nucleic acid molecules encoding conservatively or non-conservatively amino acid substituted, inserted, or deleted variants of SEQ ID NO: 2. This rejection is meant to encompass any and/or all embodiments of the claims other than a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1 or the nucleotide sequence of the insert of the deposited clone, or a nucleic acid molecule encoding the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence encoded by the deposited clone. In some instances the claims require that the polypeptide encoded by the claimed nucleic acid molecule possess an activity that is possessed

by the polypeptide of SEQ ID NO: 2 or possess antigenic properties. However, the claims do not require that the polypeptide possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Simply describing a large genus of any and/or all potential activities, as in, "an activity that is possessed by the polypeptide of SEQ ID NO: 2", is not sufficient to describe a particular biological activity. Nor does such a description lead those skilled in the art to a particular activity. The property of being "antigenic" says nothing regarding the particular antigenicity of the polypeptide or fragment. Furthermore, Galzie (u8) teaches that FGFs represent a group of polypeptide mitogens eliciting a wide variety of responses, that their roles are far more extensive than the name "FGF" implies, and that not all FGFs are mitogenic for fibroblasts (page 669, Abstract and paragraph bridging columns 1-2). Therefore, knowledge of one FGF's structure and function does not provide predictability about function of a structurally related FGF. Furthermore, there are no working examples of such variant polynucleotides and polypeptides. The specification lacks guidance for the amino acids in SEQ ID NO: 2 that are essential for its biological activity and structural integrity and those amino acids that are either expendable or substitutable. The skilled artisan is left to extensive experimentation wherein such variant polynucleotides and polypeptides are randomly made and through trial and error experimentation is left to determine how such variants can be used. Moreover, there is a lack of predictability in the art. Predicting structure, hence function, from primary amino acid sequence data is extremely complex and there doesn't exist an efficient algorithm for predicting the structure of a given protein from its amino acid sequence alone. See Bowie (w8) page 1306, column 1, full paragraph 1, or Ngo (x8) page 433, full paragraph 1, and page 492, full paragraph 2.

In view of the breadth of the claims, the limited amount of direction and working examples provided by the inventor, the unpredictability in the art and the quantity of experimentation needed to make or use the invention based on the content of the disclosure, it would require undue experimentation for the skilled artisan to make and/or use the full scope of the claimed invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

The following claims are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1-8, 10, 11, 44 are indefinite over the recitation of "moderately or highly stringent conditions" because stringency varies according to the hybridization conditions and the particular hybrid under study. The specification fails to precisely define "moderately or highly stringent conditions". One of ordinary skill in the art would not be reasonably apprised of the metes and bounds of the invention. The metes and bounds are not clearly set forth.

Claims 8, 10 are indefinite because they recite the term "FGF-L polypeptide". Because the instant specification does not identify that material element or combination of elements which is unique to, and, therefore, definitive of "FGF-L polypeptide" an artisan cannot determine what additional or material limitations are placed upon a claim by the presence of this element. The metes and bounds are not clearly set forth.

Claims 2-8, 10, 11, 44 are indefinite over the recitation of "an activity" of the polypeptide set forth in SEQ ID NO: 2. Because the instant specification does not identify that material element or combination of elements which is unique to, and, therefore, definitive of "an activity" an artisan cannot determine what additional or material limitations are placed upon a claim by the presence of this element. The metes and bounds are not clearly set forth. It is unclear what activity is intended.

Claims 1-8, 10, 11, 44 are indefinite over the recitation of "complementary to" because it is unclear if a nucleotide sequence that is a full length complement or a nucleotide sequence that is only complementary to some portion of a nucleic acid molecule is intended. The metes and bounds are not clearly set forth.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) do not apply to the examination of this application as the application being examined was not (1) filed on or after November 29, 2000, or (2) voluntarily published under 35 U.S.C.

122(b). Therefore, this application is examined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

Claims 3-6, 8 are rejected under 35 U.S.C. 102(a) as being anticipated by Koga (cited by Applicants). The teachings of Koga are discussed below. The terms moderately or highly stringent conditions are vague and indefinite. Koga's nucleic acid molecule would hybridize to the complement of any of 3(a)-3(e) under moderately or highly stringent conditions in the absence of evidence to the contrary.

Claims 1, 2, 4-6, 8, 11 are rejected under 35 U.S.C. 102(b) as being anticipated by Koga (cited by Applicants). Koga discloses an isolated nucleic acid molecule (page 757, Figure 1) that has a best similarity of 74.2% to SEQ ID NO: 1, as indicated below:

```
AB012615
LOCUS       AB012615               1925 bp    mRNA    linear   VRT 08-SEP-1999
DEFINITION  Xenopus laevis mRNA for XFGF-20, complete cds.
ACCESSION   AB012615
VERSION     AB012615.1  GI:5762261
KEYWORDS    XFGF-20.
SOURCE      Xenopus laevis tailbud cDNA to mRNA.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (sites)
  AUTHORS   Koga,C., Adati,N., Nakata,K., Mikoshiba,K., Furuhata,Y., Sato,S.,
            Tei,H., Sakaki,Y., Kurokawa,T., Shiokawa,K. and Yokoyama,K.K.
  TITLE     Characterization of a novel member of the FGF family, XFGF-20, in
            Xenopus laevis
  JOURNAL   Biochem. Biophys. Res. Commun. 261 (3), 756-765 (1999)
  MEDLINE   99373151
REFERENCE   2  (bases 1 to 1925)
  AUTHORS   Adati,N., Koga,C. and Yokoyama,K.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-1998) Chie Koga, The Institute of Physical and
            Chemical Research (RIKEN), Bio Resourse Center, Tsukuba Life
            Science Center; 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            (E-mail:koga@rtc.riken.go.jp, Tel:81-298-36-3612,
            Fax:81-298-36-9120)
COMMENT     Sequence updated (20-Aug-1999).
FEATURES             Location/Qualifiers
     source          1. .1925
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /dev_stage="tailbud"
     gene            1. .1925
                     /gene="XFGF-20"
     CDS             512. .1138
                     /gene="XFGF-20"
                     /codon_start=1
                     /product="XFGF-20"
                     /protein_id="BAA83474.1"
                     /db_xref="GI:5762262"
                     /translation="MAPLADVGTFLGGYDALGQVGSHFLLPPAKDSPLLFNDPLAQSE
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                    RLSRSAPSDLSHLQGILRRRQLYCRTGFHLQILPDGNVQGTRQDHSRFGILEFISVAI
                    GLVSIRGVDTGLYLGMNDKGELFGSEKLTSECIFREQFEENWYNTYSSNLYKHGDSGR
                    RYFVALNKDGTPRDGTRAKRHQKFTHFLPRPVDPEKVPELYKDLMGYS"
BASE COUNT      543 a    446 c    433 g    503 t
ORIGIN

  Query Match             26.4%;  Score 351.4;  DB 5;  Length 1925;
  Best Local Similarity   74.2%;  Pred. No. 3e-56;
  Matches  474;  Conservative    0;  Mismatches  156;  Indels    9;  Gaps    2;

Qy    609 CATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAGGGCTTGGGCCAGCA 668
          |||||||||  | |||||  || ||   ||| || || ||    || | | | ||   |||
Db    511 CATGGCTCCTCTGGCCGACGTGGGCACCTTCCTCGGTGGGTATGATGCCCTTGG---GCA 567

Qy    669 GGTGGGTTCGCATTTCCTGTTGCCTCCTGCCGGGGGAGCGGCCGCCGCTGCTGGGCGAGCG 728
          ||||||  || || ||| || |||| ||||||  |||  | || | |||  |   ||| |
Db    568 GGTGGGCTCCCACTTCTTGCTGCCGCCTGCCAAGGACAGCCCCCTGCTCTTCAACGACCC 627

Qy    729 CAGGAGCGCGGCGGAGCGGAGCGCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCT 788
            |     | |||||||     ||||| ||| |      |  |  | ||  | || ||
Db    628 ACTGGCTCAGTCGGAGCGACTTTCCCGCAGCGCCC------CCTCCGACCTCTCCCATCT 681

Qy    789 GCACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCT 848
          || || ||| |||||||||| ||||||||||  | ||||||||||||||||||||| ||
Db    682 CCAGGGAATCTTGCGCCGCCGCCAGCTCTATTGTAGGACCGGCTTCCACCTGCAGATACT 741

Qy    849 GCCCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATCTTGGAATT 908
          ||| ||||| | |||||||||||| |||||||| |||||||  |||||||| | |||||
Db    742 GCCGGACGGGAACGTGCAGGGCACTCGGCAGGATCACAGCCGATTCGGTATCCTAGAATT 801

Qy    909 CATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGG 968
          ||||||||  ||  | || ||||| || ||| |||| || ||||  || || || |||||
Db    802 TATCAGTGTTGCTATTGGCCTGGTTAGCATTCGAGGGGTCGACACCGGCCTTTACCTTGG 861

Qy    969 AATGAATGACAAAGGAGAACTCTATGGATCAGAGAAACTTACTTCCGAATGCATCTTTAG 1028
          |||||||| |||||||||||  | ||||| || ||||| || ||||| ||||| ||| |
Db    862 GATGAATGATAAAGGAGAACTTTTCGGATCGGAAAAACTGACGTCCGAGTGCATTTTTCG 921

Qy   1029 GGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCTAACATATATAAACATGGAGA 1088
          ||| |||||||| |||||||||| |||||||||||||| ||  |||||||||| |||||
Db    922 GGAACAGTTTGAGGAGAACTGGTACAACACCTATTCATCAAATCTATATAAACACGGAGA 981

Qy   1089 CACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAG 1148
          | |||| ||  | || ||||| |||||||||||||| || || || |||||||| ||||
Db    982 CTCTGGACGGCGATACTTTGTAGCACTTAACAAAGATGGGACCCCTAGAGATGGCACCAG 1041

Qy   1149 GTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGT 1208
            | ||||| |||||||| || |||||||| || || ||||| || ||||| |||| |||
Db   1042 AGCTAAGAGACATCAGAAGTTCACACATTTTTTGCCCAGACCTGTCGATCCTGAAAAAGT 1101

Qy   1209 TCCAGAATTGTACAAGGACCTACTGATGTACACTTGAAG 1247
          ||| ||| | || || || ||  ||  |||| |||||
Db   1102 TCCTGAACTCTATAAAGATCTCATGGGATACAGCTGAAG 1140.
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The terms moderately or highly stringent conditions are vague and indefinite. Koga's nucleic acid molecule would hybridize to the complement of SEQ ID NO: 1 or to the complement of the deposit under moderately or highly stringent conditions in the absence of evidence to the contrary. The disclosure of Koga's nucleic acid molecule is tantamount to the disclosure of the complement thereof (page 757, paragraph bridging left and right columns). Koga's nucleic acid molecule comprises a region comprising a fragment of at least about 16 nucleotides, as indicated above, and would hybridize to the complement of Koga's nucleic acid molecule.

The polypeptide encoded by Koga's nucleic acid molecule (page 757, Figure 1) is at least about 70 percent identical to SEQ ID NO: 2 and comprises at least about 25 amino acid residues, as indicated below:

```
JC7082
fibroblast somatotropin-20 - African clawed frog
N;Alternate names: fibroblast growth factor-20
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: JC7082
R;Koga, C.; Adati, N.; Nakata, K.; Mikoshiba, K.; Furuhata, Y.; Sato, S.; Tei, H.; Sakaki, Y.; Kurokawa, T.; Shiokawa, K.;
Yokoyama, K.K.
Biochem. Biophys. Res. Commun. 261, 756-765, 1999
A;Title: Characterization of a novel member of the FGF family, XFGF-20, in Xenopus laevis.
A;Reference number: JC7082; MUID:99373151; PMID:10441498
A;Accession: JC7082
A;Molecule type: mRNA
A;Residues: 1-208 <KOG>
A;Cross-references: DDBJ:AB012615; NID:g5762261; PIDN:BAA83474.1; PID:g5762262
C;Superfamily: fibroblast growth factor
C;Keywords: differentiation; fibroblast; growth factor; heparin binding

  Query Match            80.9%;  Score 904.5;  DB 2;  Length 208;
  Best Local Similarity  80.6%;  Pred. No. 1.4e-77;
  Matches  170;  Conservative   19;  Mismatches   19;  Indels    3;  Gaps    2;

Qy       1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
           |||||:|| |||| : || |||||||||| : | |  :  : :|| :|  |  : |:||
Db       1 MAPLADVGTFLGGYDALG-QVGSHFLLPPAKDSPLLFNDPLAQSERLSRSAP--SDLSHL 57

Qy      61 HGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISVAVGLVSIRGVDSGLYLG 120
             |||||||||||||||||||:|||||||| ||||||||||:||||||||:|||||
Db      58 QGILRRRQLYCRTGFHLQILPDGNVQGTRQDHSRFGILEFISVAIGLVSIRGVDTGLYLG 117

Qy     121 MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGAR 180
           .  |||||||:|||||||||||||||||||||||||:|||||:|||||||||||||||| |
Db     118 MNDKGELFGSEKLTSECIFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRDGTR 177

Qy     181 SKRHQKFTHFLPRPVDPERVPELYKDLLMYT 211
           :|||||||||||||||:||||||||: |:
Db     178 AKRHQKFTHFLPRPVDPEKVPELYKDLMGYS 208.
```

The ability to determine percent identity by a given computer program is viewed as a product-by-process limitation. The recitation of a process limitation is not viewed as positively limiting the claimed product absent a showing that the process imparts a novel property to the claimed product, as it is assumed that equivalent products are obtainable by multiple computer programs.

Koga also discloses a vector comprising the isolated nucleic acid molecule (page 757, paragraph bridging left and right columns; page 760, left column full paragraph 1), a eukaryotic host cell comprising the vector, and a process for producing the encoded polypeptide comprising culturing the host cell (page 762, left column, last full paragraph).

Claims 1-8, 10, 11, 44 are rejected under 35 U.S.C. 102(e) as being anticipated by Jeffers (a8). This rejection is based upon an effective filing date of Jeffers of July 27 1999. Jeffers teaches an isolated nucleic acid molecule (SEQ ID NO: 1) that is 99.8% identical to the present application's SEQ ID NO: 1, as indicated below:

```
US-09-817-814-1
; Sequence 1, Application US/09817814
; Patent No. US20020058036A1
; GENERAL INFORMATION:
;  APPLICANT: Jeffers, Michael
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Sudhirdas, Prayaga K
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Yang, Meija
;  APPLICANT:  Burgess, Catherine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Hermann, John L
;  APPLICANT:  LaRochelle, William J
;  APPLICANT:  Lichenstein, Henri
;  TITLE OF INVENTION: No. US20020058036A1el Fibroblast Growth Factor and Nucleic Acids
;  TITLE OF INVENTION:  Encoding Same
;  FILE REFERENCE: 15966-557 CIP2
;  CURRENT APPLICATION NUMBER: US/09/817,814
;  CURRENT FILING DATE:  2001-03-26
;  PRIOR APPLICATION NUMBER: 09/609,543
;  PRIOR FILING DATE: 2000-07-03
;  PRIOR APPLICATION NUMBER: 09/494,585
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/145,899
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 633
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-817-814-1

  Query Match            47.5%;  Score 631.4;  DB 10;  Length 633;
  Best Local Similarity  99.8%;  Pred. No. 5.6e-159;
  Matches  632;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    610 ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAGGGCTTGGGCCAGCAG 669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAGGGCTTGGGCCAGCAG 60

Qy    670 GTGGGTTCGCATTTCCTGTTGCCTCCTGCCGGGGAGCGGCCGCCGCTGCTGGGCGAGCGC 729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGGGTTCGCATTTCCTGTTGCCTCCTGCCGGGGAGCGGCCGCCGCTGCTGGGCGAGCGC 120

Qy    730 AGGAGCGCGGCGGAGCGGAGCGCCCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTG 789
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    121 AGGAGCGCGGCGGAGCGGAGCGCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTG 180

Qy    790 CACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTG 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTG 240

Qy    850 CCCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATCTTGGAATTC 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATCTTGGAATTC 300

Qy    910 ATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGGA 969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGGA 360

Qy    970 ATGAATGACAAAGGAGAACTCTATGGATCAGAGAAACTTACTTCCGAATGCATCTTTAGG 1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAATGACAAAGGAGAACTCTATGGATCAGAGAAACTTACTTCCGAATGCATCTTTAGG 420

Qy   1030 GAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCTAACATATATAAACATGGAGAC 1089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCTAACATATATAAACATGGAGAC 480

Qy   1090 ACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGG 1149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAGATGGCGCCAGG 540

Qy   1150 TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGTT 1209
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGTT 600

Qy   1210 CCAGAATTGTACAAGGACCTACTGATGTACACT 1242
                ||||||||||||||||||||||||||||||||
Db    601 CCAGAATTGTACAAGGACCTACTGATGTACACT 633.
```

Jeffers's SEQ ID NO: 1 encodes a polypeptide that is 100% identical to the present application's SEQ ID NO: 2, as indicated below:

```
US-09-817-814-2
; Sequence 2, Application US/09817814
; Patent No. US20020058036A1
; GENERAL INFORMATION:
;  APPLICANT: Jeffers, Michael
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Sudhirdas, Prayaga K
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Yang, Meija
;  APPLICANT:  Burgess, Catherine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Hermann, John L
;  APPLICANT:  LaRochelle, William J
;  APPLICANT:  Lichenstein, Henri
;  TITLE OF INVENTION: No. US20020058036A1el Fibroblast Growth Factor and Nucleic Acids
;  TITLE OF INVENTION:  Encoding Same
;  FILE REFERENCE: 15966-557 CIP2
;  CURRENT APPLICATION NUMBER: US/09/817,814
;  CURRENT FILING DATE:  2001-03-26
;  PRIOR APPLICATION NUMBER: 09/609,543
;  PRIOR FILING DATE: 2000-07-03
;  PRIOR APPLICATION NUMBER: 09/494,585
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/145,899
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-817-814-2

  Query Match            100.0%;  Score 1118;  DB 10;  Length 211;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-110;
  Matches  211;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60

Qy     61 HGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISVAVGLVSIRGVDSGLYLG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 HGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISVAVGLVSIRGVDSGLYLG 120

Qy    121 MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGAR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGAR 180

Qy    181 SKRHQKFTHFLPRPVDPERVPELYKDLLMYT 211
          |||||||||||||||||||||||||||||||
Db    181 SKRHQKFTHFLPRPVDPERVPELYKDLLMYT 211
```

Jeffers also discloses vectors containing these nucleic acids and host cells transformed with the FGF-CX nucleic acids (page 5, paragraph 64), the complement of SEQ ID NO: 1 (paragraph 83), FGF-CX polypeptides encoded by allelic variants and single nucleotide polymorphisms of FGF-CX nucleic acids and homologous nucleic acid sequences that encode conservative amino acid substitutions (paragraphs 7, 94, 100), introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NO:1,

such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein (paragraphs 109-115, 133), recombinant expression vectors designed for expression of FGF-CX in prokaryotic or eukaryotic cells (paragraph 223), viral vectors (paragraph 221), prokaryotic or eukaryotic host cells (paragraph 233), methods for producing FGF-CX protein using the host cells (paragraph 236), and promoters, enhancers and other expression control elements (paragraph 222).

Claims 1-5, 7 are rejected under 35 U.S.C. 102(b) as being anticipated by Hillier (cited by Applicants). Hillier discloses an isolated nucleic acid molecule that is fully within the metes and bounds of the embodiments of the present invention that are claim 1(d), 1(e), 2(c), 2(d), 2(e), 2(f), 3(e), 3(f), 3(g), 3(h), a vector comprising the nucleic acid molecule, and a prokaryotic host cell comprising the vector, as indicated below:

```
AA232729
LOCUS       AA232729               496 bp    mRNA    linear   EST 06-AUG-1997
DEFINITION  zr75g09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:669280
            5', mRNA sequence.
ACCESSION   AA232729
VERSION     AA232729.1  GI:1855722
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 805   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 469.
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Homo sapiens"
                     /db_xref="GDB:5563247"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:669280"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
```

```
                    Site_2: Eco RI; Equal amounts of plasmid DNA from three
                    normalized libraries (melanocyte 2NbHM, pregnant uterus
                    NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                    were made in vitro. Following HAP purification, this DNA
                    was used as tracer in a subtractive hybridization
                    reaction. The driver was PCR-amplified cDNAs from pools of
                    5,000 clones made from the same 3 libraries. The pools
                    consisted of I.M.A.G.E. clones 260232-265223,
                    340488-345479, and 484488-489479."
BASE COUNT      128 a    132 c    135 g    101 t
ORIGIN

  Query Match             37.1%;  Score 492.8;  DB 9;  Length 496;
  Best Local Similarity   99.6%;  Pred. No. 2.3e-119;
  Matches  494;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TACACGGCCGCAGCTGAACAGCATCACCGCTGTCCCAAGGACAACCCCAAAGAGGGGCCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TACACGGCCGCAGCTGAACAGCATCACCGCTGTCCCAAGGACAACCCCAAAGAGGGGCCT 60

Qy     61 CGACTGCACCTCCTCGAAGTTGCTGGCTGGCTTTGGCAAGTGCAGGAATGGTGTTTTGTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGACTGCACCTCCTCGAAGTTGCTGGCTGGCTTTGGCAAGTGCAGGAATGGTGTTTTGTG 120

Qy    121 AGGGCATGGATGGAGAAGTGCCAAGGGCCCCTGTTTGGTCACTTCCGAAGAGCAAAAACG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGGCATGGATGGAGAAGTGCCAAGGGCCCCTGTTTGGTCACTTCCGAAGAGCAAAAACG 180

Qy    181 TGTTGAGAGGAGACCGGTTTAAGATTTCAAACAGAACCTCCCCAGCGCGCATGAAAGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTTGAGAGGAGACCGGTTTAAGATTTCAAACAGAACCTCCCCAGCGCGCATGAAAGGAC 240

Qy    241 TTGATTAGCATATGTCAAGAGGACCCGCTTATATACTCGGTGTGTATGTACACAGGACTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTGATTAGCATATGTCAAGAGGACCCGCTTATATACTCGGTGTGTATGTACACAGGACTC 300

Qy    301 TGATCTGATCAGTTTGCGGAATTGGAGCCCCAGCCAACAGCCCTAGTCCTAGTATTGGCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGATCTGATCAGTTTGCGGAATTGGAGCCCCAGCCAACAGCCCTAGTCCTAGTATTGGCA 360

Qy    361 GCGGCAGCTATAGATATTTCTGCAGAGCCAGCAGCCGGCTCCCACCTACCCAAGGAGAGA 420
          ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCGGCACGTATAGATATTTCTGCAGAGCCAGCAGCCGGCTCCCACCTACCCAAGGAGAGA 420

Qy    421 AGATCGCTCCAAGACAGTGAGAGCTTCCCTGCCATTTCAGTGCAAAGTCCCTCCGGAGCG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGATCGCTCCAAGACAGTGAGAGCTTCCCTGCCATTTCAGTGCAAAGTCCCTCCGGAGCG 480

Qy    481 ACCTCAGAGGAGTAAC 496
          ||||||||||||||||
Db    481 ACCTCAGAGGAGTAAC 496.
```

Embodiment 2(c) of the present does not require any particular 25 amino acids, and any 25 amino acid polypeptide would be antigenic in the absence of evidence to the contrary. The metes and bounds of "activity" are not clearly set forth. Any 25 amino acid polypeptide would have an "activity" of the present application's SEQ ID NO: 2, in the absence of evidence to the contrary and in the absence of a clear definition of what "activity" is intended.

Hillier's nucleic acid molecule encodes a 25 amino acid polypeptide, as indicated below:

```
5'3' Frame 1


tacacggccgcagctgaacagcatcaccgctgtcccaaggacaaccccaaagaggggcct

 Y  T  A  A  A  E  Q  H  H  R  C  P  K  D  N  P  K  E  G  P

cgactgcacctcctcgaagttgctggctggctttggcaagtgcaggaatggtgttttgtg

 R  L  H  L  L  E  V  A  G  W  L  W  Q  V  Q  E  W  C  F  V

agggcatggatggagaagtgccaagggccctgtttggtcacttccgaagagcaaaaacg

 R  A  W  M  E  K  C  Q  G  P  L  F  G  H  F  R  R  A  K  T
```

```
tgttgagaggagaccggtttaagatttcaaacagaacctccccagcgcgcatgaaaggac
 C - E E T G L R F Q T E P P Q R A - K D
ttgattagcatatgtcaagaggacccgcttatatactcggtgtgtatgtacacaggactc
 L I S I C Q E D P L I Y S V C M Y T G L
tgatctgatcagtttgcggaattggagccccagccaacagccctagtcctagtattggca
 - S D Q F A E L E P Q P T A L V L V L A
gcggcacgtatagatatttctgcagagccagcagccggctcccacctacccaaggagaga
 A A R I D I S A E P A A G S H L P K E R
agatcgctccaagacagtgagagcttccctgccatttcagtgcaaagtccctccggagcg
 R S L Q D S E S F P A I S V Q S P S G A
acctcagaggagtaac
 T S E E - .
```

Embodiment 3(e) of the present invention encompasses essentially any and/or all nucleic acid molecules encoding any and/or all polypeptides.

Claims 3-10, 44 are rejected under 35 U.S.C. 102(b) as being anticipated by Nathans (b8). Embodiment 3(e) of the present invention encompasses essentially any and/or all nucleic acid molecules encoding any and/or all polypeptides. Nathans teaches an isolated nucleic acid molecule encoding a polypeptide, a viral vector comprising the nucleic acid molecule, eukaryotic and prokaryotic host cells comprising the vector, and methods of making the encoded polypeptide (Figure 1; column 6, last full paragraph; column 7, full paragraphs 1-3; column 12, full paragraph 2).

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-8, 10, 11, 44 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility.

The claims are directed to or encompass nucleic acid molecules encoding the amino acid sequence of SEQ ID NO: 2 (FGF-L) or variants of SEQ ID NO: 2 and variants of such nucleic acid molecules. The specification adequately describes nucleic acid molecules encoding the amino acid sequence of SEQ ID NO: 2. The specification asserts that the FGF-L nucleic acid molecules, polypeptides, and agonists and antagonists thereof of the present invention are useful for the same purposes for which members of the FGF family of polypeptides are known to be useful (paragraph bridging pages 73-74. The specification also discloses that the FGF-L gene appears to be most closely related to the FGF-9 and FGF-16 genes and, accordingly, FGF-L nucleic acid molecules, polypeptides, and agonists and antagonists thereof may be used to treat, diagnose, ameliorate, or prevent diseases, disorders, or conditions involving the central nervous system, teeth, brown adipose tissue, heart, or liver. See paragraph bridging pages 74-75.

However, the specification fails to disclose a specific biological role of FGF-L or its significance. After further research, a specific and substantial credible utility might be found for the claimed isolated compositions. This further characterization, however, is part of the act of invention and until it has been undertaken, Applicant's claimed invention is incomplete.

The instant situation is directly analogous to that which was addressed in Brenner v. Manson, 148 U.S.P.Q. 689 (1966), in which a novel compound which was structurally analogous to other compounds which were known to possess anti-tumor activity was alleged to be potentially useful as an anti-tumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S.C. §101, which

requires that an invention must have either an immediately apparent or fully disclosed "real world" utility. The court held that: The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility. . . . [u]nless and until a process is refined and developed to this point-where specific benefit exists in currently available form-there is insufficient justification for permitting an applicant to engross what may prove to be a broad field. . . . a patent is not a hunting license. . . .[i]t is not a reward for the search, but compensation for its successful conclusion.

Furthermore, Galzie (u8) teaches that FGFs represent a group of polypeptide mitogens eliciting a wide variety of responses, that their roles are far more extensive than the name "FGF" implies, and that not all FGFs are mitogenic for fibroblasts (page 669, Abstract and paragraph bridging columns 1-2). Furthermore, Koga (cited by Applicants) discloses that the expression pattern of FGF-20 in adult organs and tissues is different from that of FGF-9 (page 761, paragraph bridging left and right columns). Galzie and Koga are evidence that FGF family members lack a common utility applicable to all members of this family. Furthermore, one skilled in the art recognizes that although structural similarity can serve to classify a protein as related to other known proteins this classification is insufficient to establish a function or biological significance for the protein because ancient duplications and rearrangements of protein-coding segments have resulted in complex gene family relationships. Duplications can be tandem or dispersed and can involve entire coding regions or modules that correspond to folded protein domains. As a result, gene products may acquire new specificities, altered recognition properties, or modified functions. Extreme proliferation of some families within an

organism, perhaps at the expense of other families, may correspond to functional innovations during evolution. See Henikoff (v8), page 609, Abstract. Accordingly, one skilled in the art would not accept mere homology as establishing a function of protein because gene products may acquire new specificities, altered recognition properties, or modified functions. Rather, homology complements experimental data accumulated for the homologous protein in understanding the homologous protein's biological role. Although, the presence of a protein module in a protein of interest adds potential insight into its function and guides experiments, insight into the biological function of a protein cannot be automated. However, homology can be used to guide further research. See Henikoff (v8), paragraph bridging pages 613-614, through page 614, paragraph bridging columns 1-2.

The instant claims encompass a protein of as yet undetermined function or biological significance. There is no evidence of record or any line of reasoning that would support a conclusion that the FGF-L polypeptide of the instant application was, as of the filing date, useful in a manner envisioned by the application. Until some actual and specific significance can be attributed to the protein identified in the specification as FGF-L, or the gene encoding it, one of ordinary skill in the art would be required to perform additional experimentation in order to determine how to use it. Thus, there was no immediately apparent or "real world" utility for FGF-L as of the filing date. In the absence of knowledge of the biological significance of this protein, there is no immediately evident patentable use for it. To employ a protein of the instant invention in any of the disclosed uses would clearly be using it as the object of further research. Such a use has been determined by the courts to be a utility which, alone, does not support

patentability. Since the instant specification does not disclose a "real world" use for FGF-L, then there is no disclosed "real world" use for nucleic acid molecules encoding FGF-L.

Moreover, use of the claimed polynucleotide in an array is only useful in the sense that the information that is gained from the array is dependent on the pattern derived from the array, and says nothing with regard to each individual member of the array. This is a utility which would apply to virtually ever member of a general class of materials, such as any collection of proteins or DNA. Even if the expression of Appellants' individual polynucleotide is affected by a test compound in an array, the specification does not disclose any specific and substantial interpretation for the result, and none is known in the art. Given this consideration, the individually claimed polynucleotide has no "well-established" use. The artisan is required to perform further experimentation on the claimed material itself in order to determine to what "use" any expression information regarding this nucleic acid could be put.

Claims 1-8, 10, 11, 44 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Recent Statutory Changes to 35 U.S.C. § 102(e)

On November 2, 2002, President Bush signed the 21st Century Department of Justice Appropriations Authorization Act (H.R. 2215) (Pub. L. 107-273, 116 Stat. 1758 (2002)), which further amended 35 U.S.C. § 102(e), as revised by the American Inventors Protection Act of 1999 (AIPA) (Pub. L. 106-113, 113 Stat. 1501 (1999)). The revised provisions in 35 U.S.C. § 102(e) are completely retroactive and effective immediately for all applications being examined or patents being reexamined. Until all of the Office's automated systems are updated to reflect the revised statute, citation to the revised statute in Office actions is provided by this attachment. This attachment also

substitutes for any citation of the text of 35 U.S.C. § 102(e), if made, in the attached Office action.

The following is a quotation of the appropriate paragraph of 35 U.S.C. § 102 in view of the AIPA and H.R. 2215 that forms the basis for the rejections under this section made in the attached Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

35 U.S.C. § 102(e), as revised by the AIPA and H.R. 2215, applies to all qualifying references, except when the reference is a U.S. patent resulting directly or indirectly from an international application filed before November 29, 2000. For such patents, the prior art date is determined under 35 U.S.C. § 102(e) as it existed prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. § 102(e)).

The following is a quotation of the appropriate paragraph of 35 U.S.C. § 102 prior to the amendment by the AIPA that forms the basis for the rejections under this section made in the attached Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

For more information on revised 35 U.S.C. § 102(e) visit the USPTO website at www.uspto.gov or call the Office of Patent Legal Administration at (703) 305-1622.

Conclusion

No claims are allowable.

ANY INQUIRY CONCERNING THIS COMMUNICATION OR EARLIER COMMUNICATIONS FROM THE EXAMINER SHOULD BE DIRECTED TO DAVID S. ROMEO WHOSE TELEPHONE NUMBER IS (703) 305-4050. THE EXAMINER CAN NORMALLY BE REACHED ON MONDAY THROUGH FRIDAY FROM 7:30 A.M. TO 4:00 P.M.

IF ATTEMPTS TO REACH THE EXAMINER BY TELEPHONE ARE UNSUCCESSFUL, THE EXAMINER'S SUPERVISOR, GARY KUNZ, CAN BE REACHED ON (703) 308-4623.

IF SUBMITTING OFFICIAL CORRESPONDENCE BY FAX, APPLICANTS ARE ENCOURAGED TO SUBMIT OFFICIAL CORRESPONDENCE TO THE FOLLOWING TC 1600 BEFORE AND AFTER FINAL RIGHTFAX NUMBERS:

BEFORE FINAL (703) 872-9306
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CUSTOMERS ARE ALSO ADVISED TO USE CERTIFICATE OF FACSIMILE PROCEDURES WHEN SUBMITTING A REPLY TO A NON-FINAL OR FINAL OFFICE ACTION BY FACSIMILE (SEE 37 CFR 1.6 AND 1.8).

FAXED DRAFT OR INFORMAL COMMUNICATIONS SHOULD BE DIRECTED TO THE EXAMINER AT (703) 308-0294.

ANY INQUIRY OF A GENERAL NATURE OR RELATING TO THE STATUS OF THIS APPLICATION OR PROCEEDING SHOULD BE DIRECTED TO THE GROUP RECEPTIONIST WHOSE TELEPHONE NUMBER IS (703) 308-0196.

DAVID ROMEO
PRIMARY EXAMINER
ART UNIT 1647

DSR
JANUARY 13, 2003